

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:04:33 ; Search time 18 Seconds
(without alignments)
1276.451 Million cell updates/sec

Title: US-09-887-784-4
Perfect score: 1274
Sequence: 1 MVSKEELFGVVPILVELD.....VLIGFVTAAGITLGMDELYK 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1241	97.4	238	1 J01514	green-fluorescent
2	105	8.2	785	2 H72228	hypothetical prote
3	91.5	7.2	861	2 H64102	leucine-trna ligas
4	90	7.1	632	2 T06586	DNA-binding protei
5	89.5	7.0	887	2 E82590	leucyl-trna synthet
6	88.5	6.9	655	2 D83917	DNA topoisomerase
7	87.5	6.9	370	2 E70390	iron-sulfur cofact
8	87.5	6.9	860	2 AC0582	leucyl-trna synthet
9	87.5	6.9	2222	1 A36028	DNA-directed DNA p
10	87.5	6.9	2573	2 D71614	hypothetical prote
11	87	6.8	578	1 I40794	dihydrolipeamide d
12	86.5	6.8	874	2 JC4930	S-layer protein pr
13	86.5	6.8	797	2 JC4078	protective surface
14	86.5	6.8	808	2 F64102	protective surface
15	86	6.8	357	2 G81355	trna (uracil-5)-m
16	85.5	6.7	788	1 J0VLRH	DNA-directed DNA p
17	85.5	6.7	889	2 JC3576	inter-alpha-trypsi
18	85.5	6.7	941	2 S29043	cellulase (EC 3.2.
19	85	6.7	281	2 AD2052	hypothetical prote
20	85	6.7	439	2 JH0414	synaptogamin o-p65
21	84.5	6.6	425	2 C97354	hypothetical prote
22	84.5	6.6	613	2 A95552	oligoendopeptidase
23	84	6.6	353	2 E84941	imidazoleglycerol-
24	83.5	6.6	836	1 J0VLD	DNA-directed DNA p
25	83.5	6.6	1134	2 A60234	Iga Fc receptor pr
26	83.5	6.6	1164	1 FCSOAG	Iga Fc receptor pr
27	83	6.6	461	2 T06936	photosystem II chl
28	83	6.5	471	2 T27856	hypothetical prote
29	83	6.5	774	2 T39539	alpha-amylase homo

30	82.5	6.5	534	1 NICLMA	nitrogenase (EC 1.
31	82.5	6.5	740	2 G95153	neuraminidase, pro
32	82	6.4	682	2 D90946	hypothetical prote
33	82	6.4	682	2 H85794	hypothetical prote
34	82	6.4	682	2 A41798	carboxy-terminal p
35	82	6.4	752	1 KARTCL	proprotein convert
36	82	6.4	865	2 T11852	lipoygenase (EC 1
37	81.5	6.4	263	2 S53488	water-stress-induc
38	81.5	6.4	310	2 S68225	synerghomototropi
39	81.5	6.4	1983	2 G86643	hypothetical prote
40	81	6.4	336	2 C64468	hypothetical prote
41	81	6.4	355	2 S76940	hypothetical prote
42	81	6.4	734	2 T13674	hypothetical prote
43	81	6.4	743	2 T13673	hypothetical prote
44	81	6.4	1224	1 ERHUAH	coatamer complex a
45	80.5	6.3	393	2 C64613	conserved hypothet

ALIGNMENTS

RESULT 1

J01514

green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)

C:Species: Aequorea victoria

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_Change 23-Mar-2001

C:Accession: J50692; J01514; P00335; S48693; S51330; S51331

R:Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.

Gene 111, 229-233, 1992

A:Title: Primary structure of the Aequorea victoria green-fluorescent protein.

A:Reference number: J01514; MUID:9217527; PMID:1347277

A:Accession: J50692

A:Molecule type: DNA

A:Residues: 1-107, 'S', 109-238 <PRA1>

A:Cross-references: GB:M62654; NID:g155663; PIDN:AAA27722.1; PID:g155663

A:Accession: J01514

A:Molecule type: mRNA

A:Residues: 1-99, 'F', 101-140, 'L', 142-218, 'V', 220-238 <PRA2>

A:Cross-references: GB:M62653; NID:g155660; PIDN:AAA27721.1; PID:g155661

A:Accession: P00335

A:Molecule type: protein

A:Residues: 46-64, 74-122, 132-151, 154-183, 185-200 <PRA3>

R:Inouye, S.; Tsuji, F.I.

FEBS Lett. 351, 211-214, 1994

A:Title: Evidence for redox forms of the Aequorea green fluorescent protein.

A:Reference number: S48693; MUID:94364470; PMID:8082767

A:Accession: S48693

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-24, 'Q', 26-156, 'P', 158-171, 'K', 173-238 <INO>

A:Cross-references: GB:L29345; NID:g606383; PIDN:AAA58246.1; PID:g606384

R:Watkins, J.N.; Campbell, A.K.

submitted to the EMBL data library, January 1995

A:Reference number: S51330

A:Accession: S51330

A:Molecule type: mRNA

A:Residues: 1-13, 'V', 15-24, 'Q', 26-44, 'N', 46-153, 'G', 155-156, 'P', 158-171, 'K', 173-237

A:Cross-references: EMBL:X83959; NID:9634008; PIDN:CAA58789.1; PID:g634009

A:Experimental source: clone gfp1

A:Accession: S51331

A:Molecule type: mRNA

A:Residues: 1-24, 'Q', 26-29, 'R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208

A:Cross-references: EMBL:X83960; NID:9634010; PIDN:CAA58790.1; PID:g634011

A:Experimental source: clone gfp2

R:Yang, F.; Moss, L.G.; Phillips Jr., G.N.

submitted to the Brookhaven Protein Data Bank, August 1996

A:Reference number: A56592; PDB:1GFL

A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A', 2-79, 'R'

A>Note: engineered sequence based on J01514, cloned and expressed in Escherichia cc

Nat. Biotechnol. 14, 1246-1251, 1996

A:Title: The molecular structure of green fluorescent protein.

A:Reference number: A58953; MUID:98294543; PMID:9631087

A:Contents: annotation; X-ray crystallography, 1.9 angstroms
C:Comment: this protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emitting
C:Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-
C:Genetics:
A:Gene: GFP

A:Introns: 69/3; 167/3

C:Superfamily: green-fluorescent protein

C:Keywords: chromoprotein; luminescence

F:65-67/Cross-link: 5-Imidazolilone (Ser-Gly) #status experimental

F:66/Modified site: dehydrotyrosine (Tyr) #status experimental

Query Match 97.4%; Score 1241; DB 1; Length 238;

Best Local Similarity 97.1%; Pred. No. 8.3e-97;

Matches 231; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDNGHFKFSVSGEGDGYGKLTAKFICTTGKLPVWPPTL 61

DB 1 MSKGEELFTGVVPIVLVDGVDNGHFKFSVSGEGDGYGKLTAKFICTTGKLPVWPPTL 60

QY 62 VTTLSGVQCFSPYDPHMKQHDFFKSPAMPEGVVQERTIFFKDDGNYKTRAEVKFEGDTLV 121

DB 61 VTFSGVQCFSPYDPHMKQHDFFKSPAMPEGVVQERTIFFKDDGNYKTRAEVKFEGDTLV 120

QY 122 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRHNIEDGVSQVLAD 181

DB 121 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRHNIEDGVSQVLAD 180

QY 182 HYQONTPIGDPVLLPDNHYLSTQSNLSKDPNKRDNVLLGFVTAAGTILGMDLYK 239

DB 181 HYQONTPIGDPVLLPDNHYLSTQSNLSKDPNKRDNVLLGFVTAAGTILGMDLYK 238

RESULT 2

H72228

hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)

C:Species: thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: H72228

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: H72228

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-785 <ARN>

A:Cross-references: GB:AE001806; GB:AE000512; NID:g4982196; PIDN:AAD36691.1; PTD:g498219

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1624

Query Match

Best Local Similarity 8.2%; Score 105; DB 2; Length 785;

Matches 46; Conservative 32; Mismatches 71; Indels 84; Gaps 7;

QY 3 SKGEELFTGVVPIVLVDGVDNGHFKFSVSGEGDGYGKLTAKFICTTGKLPVWPPTLV 62

DB 15 NSGRSFEGTVPVQVQAD-----LVKGLLPVYVGM- 46

QY 63 TTTLSGVQCFSPYDPHMKQHDFFKSPAMPEGVVQERTIFFKDDGNYKTRAEVKFEGDTLVN 122

DB 47 -----NEDLKEIEDREWIYEFEEFKEDVKEGERVDLVFEGDTLS 88

QY 123 RIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRHNIEDGVSQVLADH 182

DB 89 DYLVNGVYL---GSTEDMFIERYFDYTNVL---KEKNHLKYIK-----SPIRVFPT 134

QY 183 YQONTPIGDPVLLPDNHYLSTQSNLSKDPNKRDNVLLGFVTAAGTILGMD 235

DB 135 LEQNTGVVLGGP-----EDP-----IRGVIRKAOYSYGMW 163

RESULT 3

H64102

leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)

N:Alternate names: leucyl-tRNA synthetase

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002

C:Accession: H64102

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavac

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidm

; D.M.; Brandon, R.C.; Fine, L.D.; Frichman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vent

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: H64102

A:Molecule type: DNA

A:Residues: 1-961 <TIGR>

A:Cross-references: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1; PID:g157394

C:Genetics:

A:Gene: leuS

C:Superfamily: leucine-tRNA ligase

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 7.2%; Score 91.5; DB 2; Length 861;

Best Local Similarity 24.1%; Pred. No. 13;

Matches 46; Conservative 26; Mismatches 60; Indels 59; Gaps 11;

QY 50 TTKGLPVPWPTLVTTLSYGVQCFSPYDPHMKQHDFFKSPAMPEGVVQERTIFFKDDGNYKTRAEVKFEGDTLV 103

DB 314 TQDKLPI-WVANFVLMHYGTGAVMAVPAH-DQDQD-----EFAQKYSLPKQVIAPLA 364

QY 104 DGNKTRAEVFEQDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNYIMADK-QKNGI 162

DB 365 DEEDLTQKQAFVEHCKLVNSDEFGKNP--DGAFNG-----TADKLEKGV 408

QY 163 ---KVNFKIRH-----NIEGDSVOLADHYQONTPIGDPVLLPDNHYL- 202

DB 409 GKQVNYLRDMGVSQRQYWGAPIMLTLENGDVVPA-----PMEDLPILPDDVYMD 461

QY 203 STQSALSQDPN 213

DB 462 GVKSPINADPN 472

RESULT 4

T06586

DNA-binding protein PD2 - garden pea

C:Species: pisum sativum (garden pea)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999

C:Accession: T06586

R:Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.

submitted to the EMBL Data Library, June 1996

A:Description: Identification of a novel family of DNA-binding proteins with two AT-

A:Reference number: Z15774

A:Accession: T06586

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-632 <SAT>

A:Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185

A:Experimental source: cv. Alaska

Query Match

Best Local Similarity 7.1%; Score 90; DB 2; Length 632;

Matches 49; Conservative 26; Mismatches 79; Indels 56; Gaps 7;

QY 16 LVLELDGVNGHFKFSVSGEGDGYGKLTAKFICTTGKLPVWPPTLVTTLSYGVQCFSPY 75

DB 363 IVQDGRVDGSKVDVINKESNEATIPENK---PTEPKLDVEQEALNATM----- 408

QY 76 PDHMKQHDFFKSPAMPEGVV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIE 125

Db 409 PSSAKVNLTKDLIVETFPPLRSVARTSSGREGSEELKDSGSLERDTKKLEBOGKNS-E 467
QY 126 LKGIIDPKEDGNILGHKLE-----YNNHNVYIMADKQ-----N 160
Db 468 LKGIETPDNSTLDERFENALGNKILKEISNPRHDVESANHSHTNKOQTVSHOKAETNN 527
QY 161 GIKVNFKIRHNIEDG-----SVQLADHYQ 184
Db 528 QSQVEDVAKNIQDDSKPSESLHAKDKYR 557

RESULT 5
E82590
leucyl-tRNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: E82590
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: E82590
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-887 <SIM>
A:Cross-references: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.P.; Brimnes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.; Marino, C.L.; Marques, M.V.; Martins, H. A:Authors: Martins, E.M.F.; Matsukuma, A.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sancelli, R.V.; Savaas M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2176
C:Superfamily: leucine-tRNA ligase

Query Match 7.0%; Score 89.5; DB 2; Length 887;
Best Local Similarity 22.2%; Pred. No. 20;
Matches 44; Conservative 29; Mismatches 68; Indels 57; Gaps 10;
QY 50 TTGKLPVNPPTLTLSYGVQCFSRYPDHMKQHDFFKSAMPEGVQERTIFFKDGNY-- 107
Db 329 TNEQLPV-WYANFVLMAYGTGAVMVPFGHDQDQEF--ANKYGLPIRQVLTALKEPRNQDE 385
QY 108 -----KTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKLEYNHNVYI 153
Db 386 STWEPDVRWDYADKTR---EFE---LINSNEFDLDYQDAFEVLAERFE----- 429
QY 154 MADKQKNG-KVNFKIRHNIEDGVSQVLADHYQVQNPPI-----GDGPVLLPDN 199
Db 430 ---RQGRGQRVNYRLR----DMGVSQRQYWCGRPIPYICPTGCAVFPVPEQDLVILPEN 482
QY 200 -HYLSTQSALSKEQNEKR 216
Db 483 VAFSGTGSPIKTPDPEWRK 500

RESULT 6
DB3917
DNA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: DB3917

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: DB3917
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-655 <STO>
A:Cross-references: GB:AF001514; GB:BA000004; NID:g10174613; PIDN:BAB05859.1; GSPDB
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2140
C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

Query Match 6.9%; Score 88.5; DB 2; Length 655;
Best Local Similarity 21.9%; Pred. No. 17;
Matches 53; Conservative 37; Mismatches 95; Indels 57; Gaps 9;
QY 22 DVNGHK---FSVSGEGEGDAT---YGLKTLAFI-----CTTGKLPVWP 59
Db 63 NVTIHKDQSVSVRDEGRMGPTGMHKLKGTPEVILVLHAGGFGGGGATSGLHGVA 122
QY 60 TLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGVQER-----TIFFKDDG----- 105
Db 123 SVVNALSEWLIVELKEDGWYEQRFENGCKPSTTLEKKGKTRGTGTHFKPDPVFTST 182
QY 106 --NYKTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKLEYNHNVYIMADK----- 157
Db 183 NFNVTLSERLREAAFLKGLKLTDLRDDTKVEFH-YEDGKAFVYLNEDKTELHPV 241
QY 158 -----OKNGIKVNFKIRHNIEDGVSQVLADHYQVQNPPIGDPVLLPDNHYLSTQSALSKE 212
Db 242 VFNNGESNGIEIEFAFOFN--DGYTENVLSFVNVRKDG-----GTHELGAKTAMTRAV 294
QY 213 NE 214
Db 295 NE 296

RESULT 7
E70390
iron-sulfur cofactor synthesis protein nifs - Aquifex aeolicus
N:Contains: L-cysteine sulfoxidase (EC 2.8.1.1-)
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 07-Dec-1999
C:Accession: E70390
V. Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: E70390
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-370 <AQF>
A:Cross-references: GB:AF000720; NID:g2983529; PIDN:AAC07111.1; PID:g2983536; GB:AF
A:Experimental source: strain VF5
C:Genetics:
A:Gene: nifs1
C:Superfamily: nitrogen fixation protein nifs
C:Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase
F:195/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted
F:318/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 6.9%; Score 87.5; DB 2; Length 370;
Best Local Similarity 25.4%; Pred. No. 9.5;
Matches 49; Conservative 30; Mismatches 91; Indels 23; Gaps 8;
QY 4 KGEELFTGVV-----FILVELD-----GDVNGHKF-SVSGEG-----EGDAYGKTLKFICT 50
Db 164 KGVPLLTDAVQAIKGIPIELKNISYATFSCHKPFAIKGSGFLYSDEANVEPLVGGQE 223
QY 51 TGKLP-----VPWPTLTLSYGVQCFSRYPDHMKQ-HDFEKSAMPEGVQERTIFFKDD.104

QY 94 VQERTIFFKD--DGNKYKTRAEVKEFGDTLVNRIELKGDIFDKEDGNILGHKLEYN--YN5H 149
 Matches 34; Conservative 30; Mismatches 53; Indels 13; Gaps 5;

QY 94 VQERTIFPKD--DGNKYKTRAEVKFEGEGLTVNRIELKGFDPKEDGNILGHKLEYN--YNSH 149

Db 126 LKKEITILCKOIKSGNDPMDSEISLFDKDDMVDDKELK--DFPKSSLIKKNKEVNIYNNK 183
Qy 150 NVYIMADKQKNGKIRNIEGDSVOLADHQQOQNPIGDGPVLLPDNHYLSQSALS 209
Db 184 NLHKKENKKDEKKNKHNNNNM---ITYKNI---DKTHYILDNNVVHILNDIN 236
Qy 210 KDPNEKRDMH 219
Db 237 TYLKRERYM 246

RESULT 11
140794
diacylglycerol dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum
N:Alternate names: 2-oxoglutarate dehydrogenase complex chain E3; acetoin dehydrogenase
hydrogenase complex chain E3; S-complex 50K chain
C:Species: Clostridium magnum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: 140794
R:Kruger, N.; Oppermann, F.B.; Lorenzl, H.; Steinbuechel, A.
J. Bacteriol. 176, 3614-3630, 1994
A:Title: Biochemical and molecular characterization of the Clostridium magnum acetoin de
A:Reference number: 140793; MUID:94266715; PMID:8206840
A:Accession: 140794
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-578 <KRU>
A:CROSS-references: GB:L31844; NID:9472324; PIDN:AAA21748.1; PID:9472330
C:Function:
A:Description: catalyzes the oxidation of dihydrolipoamide to lipoamide using NAD
A:Pathway: acetoin dehydrogenase enzyme system
C:Superfamily: Alkaligenes dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase
C:Keywords: FAD; flavoprotein; lipoamide; NAD; oxidoreductase; redox-active disulfide
F:5-77/Domain: lipoyl/biotin-binding homology <LPB>
F:117-145/Region: beta-alpha-beta FAD nucleotide-binding fold
F:119-561/Domain: dihydrolipoamide dehydrogenase homology <DL>
F:287-315/Region: beta-alpha-beta NAD nucleotide-binding fold
F:153-158/Disulfide bonds: redox-active #status predicted

Query Match 6.8%; Score 87; DB 1; Length 578;
Best Local Similarity 23.5%; Pred. No. 19;
Matches 54; Conservative 40; Mismatches 84; Indels 52; Gaps 12;
Qy 10 TGVPVILVLDGVDNGHFKFSVSGEGDGYCKLTK-----FICTGKLPVWPPTLV 63
Db 255 TGSMPFPIEIE---GNKLS-----GVIST-GALSLESPESIALIGGVIGVFASIFN 305
Qy 64 TLSYGVCFSRYPDHMKQHDFFKSAMPEGVQERTIFFKDDGNYKTRAEVKFEGDILVNR 123
Db 306 SLGCKVSIITEMPLPHLPMDREISEI-----AKALIRDGMINNN 346
Qy 124 IELKIDFREDG---NILGHKLEYNYNHNYIMADKKN--GIKYNFKIRHNIEDGSVQ 178
Db 347 CKVTRLEQEDGLKVSFIDGKEESIDVEKVLAVGRSNIIEGLDVE-KIGVKTEGSI 405
Qy 179 LADHYQONT-----PIGD--GPVLLPDNHYLSQSALSKD-----PNEKRDH 218
Db 406 VNDKMETNVEGIYAGDCTGKIMLA--HVASDQGVYAAENINGQNKMDY 453

RESULT 12
JC4930
S-layer protein precursor - Bacillus licheniformis
C:Species: Bacillus licheniformis
C:Date: 22-Oct-1996 #sequence_revision 01-Nov-1996 #text_change 15-Oct-1999
C:Accession: JC4930
R:Zhu, X.; McVeigh, R.R.; Malathi, P.; Ghosh, B.K.
Gene 173, 189-194, 1996
A:Title: The complete nucleotide sequence of the Bacillus licheniformis NM105 S-layer-e
A:Reference number: JC4930; MUID:97082965; PMID:8964497
A:Accession: JC4930
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-874 <2HU>
A:CROSS-references: GB:U38842; NID:gl055336; PIDN:AA44405.1; PID:gl055337
A:Experimental source: strain NM105
C:Comment: This protein is a glycoprotein. It functions as protective coats, molecu
C:Genetics:
A:Gene: oipa
C:Superfamily: S-layer repeat homology
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-874/Product: S-layer protein #status predicted <MAT>
F:157-209/Domain: S-layer repeat homology <SLR3>

Query Match 6.8%; Score 87; DB 2; Length 874;
Best Local Similarity 22.8%; Pred. No. 32;
Matches 65; Conservative 28; Mismatches 96; Indels 96; Gaps 14;
Qy 6 EELF--TGVPVILV---VELDGDVNGHFKFSVSGEGDGYCKLTKLFI 48
Db 551 KEVFPQTGVGVKVLVDVTTNNGSICGTSIKVKGENVAGTTHFQNPASGEGYSLHVEVT 610
Qy 49 CTTGKLPVWPPTLV-----TTLSYGVQCFSRYPDHMKQHDFFKSAMPEGVQER 97
Db 611 KSNIGHEAPRLVSKAGQGEAADTTLGAGNTVAYQLSNYTTGEGVADADLAGY--EF 668
Qy 98 TIFKDDGNYKTRAEVKFEGDILVNRLEAGID--FKEDGNIILGHKLEYNYNHNYIM 154
Db 669 RV-----GNDKI-ASAKIEGTLKVTGKTAGTVDVILTKDGTATAGH-ATITVTQENQIT 721
Qy 155 AKQK-----NGIKYNFKIRHN-----IEDGSVOLADH 182
Db 722 SVRFKDEVEQFENKYNIDRVLDVVKSDKDDVLNGIKLNISTEKHVRIVDEGTEQ----- 777
Qy 183 YQONTPIGDGPVLLPDNHYLSQSALSQKDPNEKRHDHVLGFTVA 227
Db 778 -----GKV-----YLDNRDNATFDGND-----VALGYVTA 802

RESULT 13

JC4078
protective surface antigen D-15 precursor - Haemophilus influenzae (type b)
C:Species: Haemophilus influenzae
A:Variety: type b
C:Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 29-Sep-1999
C:Accession: JC4078
R:Flack, F.S.; Loomore, S.; Chong, P.; Thomas, W.R.
Gene 156, 97-99, 1995
A:Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilu
A:Reference number: JC4078; MUID:95255676; PMID:7737523
A:Accession: JC4078
A:Molecule type: DNA
A:Residues: 1-797 <FLA>
A:CROSS-references: GB:U13961; NID:9537447; PIDN:AAA85645.1; PID:9537448
A:Experimental source: type b
C:Superfamily: protective surface antigen D-15
C:Keywords: surface antigen
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-797/Product: protective surface antigen D-15 #status predicted <MAT>

Query Match 6.8%; Score 86.5; DB 2; Length 797;
Best Local Similarity 21.9%; Pred. No. 32;
Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps 11;
Qy 65 LSYGVQCFSRYPDHMKQHDFF-----FKSAMPEGVQER-----RTI 99
Db 427 IGYGTESISTQASVKQDNFLGTGAANSIAGTKNDYGSVNLGYTEPYTKDGVSLGGNV 486
Qy 100 PFKDDGNYKTRAEVKFEGDILVNRLEAGIDFKEDGNI---LGH-----KLEYNYS 148
Db 487 FFENVNDSKSDTSSNKRRTYGSNTVL-GFPVNNNSYVVGLTGHTYKINSFALEYN--- 542
Qy 149 HNYIMADKQK-NGIKYNFKIRHNIEDGSVOLADHYQ-----NTPIGDGPVLL 196
Db 543 RNLYIQSMKFKNGIKTN-----DFDSFGWYNLSNRGYFPTKGVKASIG-GRVTI 593

